

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 22, 2001, 01:26:59 ; Search time 33.83 Seconds  
(without alignments)  
6425.574 Million cell updates/sec

Title: US-09-515-806-2  
Perfect score: 1643  
Sequence: 1 MAGRGAPGRDEPPESYP.....YNIKVEKKVSLFLSYRDD 1643

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 425026 seqs, 132305027 residues

Word size: 0  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL\_16:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phase:  
10: sp\_plant:  
11: sp\_rodent:  
12: sp\_unclassified:  
13: sp\_vertebrate:  
14: sp\_virus:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1467	89.3	1495	4 Q9P2K8	Q9P2K8 homo sapien
2	932	56.7	938	4 Q9NSQ3	Q9NSQ3 homo sapien
3	785	47.8	806	4 Q9H5K1	Q9H5K1 homo sapien
4	510	31.0	548	4 Q9UJ56	Q9UJ56 homo sapien
5	185	11.3	191	4 Q9NSZ5	Q9NSZ5 homo sapien
6	85	5.2	1648	11 Q9QZ05	Q9QZ05 mus musculus
7	82	5.0	1370	11 Q9ESB8	Q9ESB8 mus musculus
8	82	5.0	1570	11 Q9ESB6	Q9ESB6 mus musculus
9	82	5.0	1648	11 Q9ESB7	Q9ESB7 mus musculus
10	14	0.9	1589	5 Q61651	Q61651 drosophila
11	14	0.9	1589	5 Q01712	Q01712 drosophila
12	14	0.9	1589	5 Q9V9X8	Q9V9X8 drosophila
13	11	0.7	576	5 Q9VWB2	Q9VWB2 drosophila
14	10	0.6	285	13 Q9DEB2	Q9DEB2 seriola qui
15	10	0.6	301	6 Q19055	Q19055 papio hamad
16	10	0.6	307	13 Q9Q458	Q9Q458 brachydanio
17	10	0.6	312	5 Q17349	Q17349 caenorhabdi
18	10	0.6	359	14 Q85453	Q85453 murine sarc
19	10	0.6	375	14 Q67624	Q67624 lc4 retrovi

20	10	0.6	420	13 Q90893	Q90893 gallus gall
21	10	0.6	421	4 Q15278	Q15278 homo sapien
22	10	0.6	462	10 Q39886	Q39886 glycine max
23	10	0.6	506	14 Q85632	Q85632 avian retro
24	10	0.6	598	13 P70032	P70032 xenopus lae
25	10	0.6	602	11 Q63485	Q63485 xenopus lae
26	10	0.6	615	5 Q20845	Q20845 caenorhabdi
27	10	0.6	632	5 Q9UA36	Q9UA36 caenorhabdi
28	10	0.6	632	5 Q9N2L7	Q9N2L7 caenorhabdi
29	10	0.6	636	5 Q9Y1J3	Q9Y1J3 caenorhabdi
30	10	0.6	648	5 Q9Y1J3	Q9Y1J3 caenorhabdi
31	10	0.6	649	5 Q9Y1J3	Q9Y1J3 caenorhabdi
32	10	0.6	651	4 Q61662	Q61662 caenorhabdi
33	10	0.6	739	5 Q9W4Z3	Q9W4Z3 homo sapien
34	10	0.6	782	5 Q9NEH9	Q9NEH9 drosophila
35	10	0.6	813	5 Q9N4E3	Q9N4E3 c. elegans
36	10	0.6	903	3 Q9HGN1	Q9HGN1 schizosacch
37	10	0.6	1106	13 Q42291	Q42291 gallus gall
38	10	0.6	1646	3 Q74297	Q74297 neurospora
39	10	0.5	1696	5 Q9XVY4	Q9XVY4 caenorhabdi
40	9	0.5	57	13 Q91566	Q91566 xenopus lae
41	9	0.5	62	5 Q9TWZ7	Q9TWZ7 lytechinus
42	9	0.5	68	13 Q90961	Q90961 gallus gall
43	9	0.5	133	5 Q9Y1Z1	Q9Y1Z1 ephydatia f
44	9	0.5	219	5 Q9Y1Y9	Q9Y1Y9 ephydatia f
45	9	0.5	226	10 Q9FFP0	Q9FFP0 arabidopsis

## ALIGNMENTS

RESULT 1

Q9P2K8  
ID Q9P2K8  
AC Q9P2K8  
PRELIMINARY; PRT; 1495 AA.  
DT 01-OCT-2000 (TREMREL. 15, Created)  
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)  
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)  
DE KIAA1338 PROTEIN (FRAGMENT).  
GN KIAA1338.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE=20181126; PubMed=10718198;  
RA Nagase T., Kikuno R., Ishikawa K., Hirose M., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes XVI.  
RT The complete sequences of 150 new cDNA clones from brain which code  
RT for large proteins in vitro."  
RL DNA Res. 7:65-73(2000).  
CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL; AB037759; BAA92576.1;  
DR InterPro; IPR000719;  
DR InterPro; IPR002064;  
DR InterPro; IPR002290;  
DR Pfam; PF00069; pkinase; 4.  
DR PROSITE; PS00116; DNA\_POLYMERASE\_B; UNKNOWN\_1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00117; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_DOM; 2.  
DR SMART; SM00220; S\_TKc; 1.  
KW ATP-binding; Serine/threonine-protein kinase; Transferase.  
FT NON\_TER  
SQ SEQUENCE 1495 AA; 169234 MW; C72723209FE038D9 CRC64;

Query Match 89.3%; Score 1467; DB 4; Length 1495;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

Db 121 ILDLGLAYIHEKGMIRDLKPNVIFLSDHVKIGDFGLATDHLAFSADSKODDGTGLIK 180  
QY 892 SDPSGHLTGMVGTALYVSEVVGSTKSAYNOKVDLFSGLIIFEMSYHPMTASERIEVL 951  
Db 181 SDPSGHLTGMVGTALYVSEVVGSTKSAYNOKVDLFSGLIIFEMSYHPMTASERIEVL 240  
QY 952 NOLRDPTSPKFFDFDDGGEHAKQKSVISWLLNHDPAKRPATATELLKSELLPPQMESESEL 1011  
Db 241 NOLRDPTSPKFFDFDDGGEHAKQKSVISWLLNHDPAKRPATATELLKSELLPPQMESESEL 300  
QY 1012 HEVLHHTLTNVGDKAYRTMMAQIFORSIPAIDYDSDILKGNFSIRFAMQOQHVCTI 1071  
Db 301 HEVLHHTLTNVGDKAYRTMMAQIFORSIPAIDYDSDILKGNFSIRFAMQOQHVCTI 360  
QY 1072 IRIFKRHGAVQLCTPLLPNRRQIYEHNEAALFMDHSGMLVMPDLRIPFARYVARNNI 1131  
Db 361 IRIFKRHGAVQLCTPLLPNRRQIYEHNEAALFMDHSGMLVMPDLRIPFARYVARNNI 420  
QY 1132 LNLKRYCIEVRFRPRKDRFHPKELLECAFDIVTSTNSFLPTAEIITVIEIIOEPFAL 1191  
Db 421 LNLKRYCIEVRFRPRKDRFHPKELLECAFDIVTSTNSFLPTAEIITVIEIIOEPFAL 480  
QY 1192 QERNYSIYNHHTMLKAILLHCGIPEDKLSQVYIILYDAVTEKTRREVEAKFCNLSLSS 1251  
Db 481 QERNYSIYNHHTMLKAILLHCGIPEDKLSQVYIILYDAVTEKTRREVEAKFCNLSLSS 540  
QY 1252 NSICRLYKFIQKGLDLOLMPNTINSILIKOKTGIAQLVKYGLKDLVEVGLLKIGIKLOV 1311  
Db 541 NSICRLYKFIQKGLDLOLMPNTINSILIKOKTGIAQLVKYGLKDLVEVGLLKIGIKLOV 600  
QY 1312 LINLGLVYKVOQHNGIIFQVAFIKRRORAVPEILAAAGRYDILLIPOFRGQALGPVPTA 1371  
Db 601 LINLGLVYKVOQHNGIIFQVAFIKRRORAVPEILAAAGRYDILLIPOFRGQALGPVPTA 660  
QY 1372 IGVSTAIDKISAVALNMEESVTISSCDLLVSVGOMSMRAINLTQKLWTAGITAEIMYD 1431  
Db 661 IGVSTAIDKISAVALNMEESVTISSCDLLVSVGOMSMRAINLTQKLWTAGITAEIMYD 720  
QY 1432 WSQSOEELQYCRHHEITYVALVSDKEGSHVKVSKFEKEROTKRVLETVDHVLOKLR 1491  
Db 721 WSQSOEELQYCRHHEITYVALVSDKEGSHVKVSKFEKEROTKRVLETVDHVLOKLR 780  
QY 1492 TKVTDERNGREASDNLAQNKGFSNAGLFEIHGATVPIVSVLAPEKLSASTRRRYE 1551  
Db 781 TKVTDERNGREASDNLAQNKGFSNAGLFEIHGATVPIVSVLAPEKLSASTRRRYE 840  
QY 1552 TOVQTRLOTSLANLHOKSSEIEILAVDLPKETILQFLSLEWDADEQAFNTTVKOLLRLP 1611  
Db 841 TOVQTRLOTSLANLHOKSSEIEILAVDLPKETILQFLSLEWDADEQAFNTTVKOLLRLP 900  
QY 1612 KORYLKLVCDEIYNIKVEKKVSVFLYSYRDD 1643  
Db 901 KORYLKLVCDEIYNIKVEKKVSVFLYSYRDD 932

RESULT 3  
Q9H5K1

ID Q9H5K1 PRELIMINARY; PRT: 806 AA.  
AC Q9H5K1;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE CDNA: FLJ23358 FIS, CLONE HEP14996.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kawabata A., Hikiiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,  
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;

\*NEDO human cDNA sequencing project.\*;  
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AK027011; BAB15625.1; - C5DBC4D2A99C4E43 CRC64;  
SQ SEQUENCE 806 AA; 92006 MW; 92006 MW;

Query Match 47.8%; Score 785; DB 4; Length 806;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 859 DDHVKIGDFGLATDHLAFSADSKODDGTGLIKSDPSGHLTGMVGTALYVSEVVGSTKS 918  
Db 16 DDHVKIGDFGLATDHLAFSADSKODDGTGLIKSDPSGHLTGMVGTALYVSEVVGSTKS 75  
QY 919 AYNOKVDLFSGLIIFEMSYHPMTASERIFVLNQLRDPTSPKFFDFDDGGEHAKQKSVI 978  
Db 76 AYNOKVDLFSGLIIFEMSYHPMTASERIFVLNQLRDPTSPKFFDFDDGGEHAKQKSVI 135  
QY 979 SWLLNHDPAKRPATATELLKSELLPPQMESESELHEVLHHTLTNVGDKAYRTMMAQIFSOR 1038  
Db 136 SWLLNHDPAKRPATATELLKSELLPPQMESESELHEVLHHTLTNVGDKAYRTMMAQIFSOR 195  
QY 1039 ISPAIDYDSDILKGNFSIRFAMQOQHVCTIIRIFKRHGAVOLCTPLLPNRRQIYEH 1098  
Db 196 ISPAIDYDSDILKGNFSIRFAMQOQHVCTIIRIFKRHGAVOLCTPLLPNRRQIYEH 255  
QY 1099 NEAALFMDHSGMLVMPDLRIPFARYVARNNLTNLRKRYCIEVRFRPRKDRFHPKELLE 1158  
Db 256 NEAALFMDHSGMLVMPDLRIPFARYVARNNLTNLRKRYCIEVRFRPRKDRFHPKELLE 315  
QY 1159 CAFDIVTSTNSFLPTAEIITVIEIIOEPFALQERNYSIYNHHTMLKAILLHCGIPED 1218  
Db 316 CAFDIVTSTNSFLPTAEIITVIEIIOEPFALQERNYSIYNHHTMLKAILLHCGIPED 375  
QY 1219 KLSQVYIILYDAVTEKTRREVEAKFCNLSNLSCLRYKFTIEQKGLDLOLMPNTINSI 1278  
Db 376 KLSQVYIILYDAVTEKTRREVEAKFCNLSNLSCLRYKFTIEQKGLDLOLMPNTINSI 435  
QY 1279 KOKTGIAQLVKYGLKDLVEVGLLKIGIKLOVLINLGLVYKVOQHNGIIFQVAFIKRR 1338  
Db 436 KOKTGIAQLVKYGLKDLVEVGLLKIGIKLOVLINLGLVYKVOQHNGIIFQVAFIKRR 495  
QY 1339 QRAVPEILAAAGRYDILLIPOFRGQALGPVPTAIGVSTADKISAVALNMEESVTISSCD 1398  
Db 496 QRAVPEILAAAGRYDILLIPOFRGQALGPVPTAIGVSTADKISAVALNMEESVTISSCD 555  
QY 1399 LLVSVGOMSMRAINLTQKLWTAGITAEIMYDWSQSOEELQYCRHHEITYVALVSDKE 1458  
Db 556 LLVSVGOMSMRAINLTQKLWTAGITAEIMYDWSQSOEELQYCRHHEITYVALVSDKE 615  
QY 1459 GSHVKVSKFEKEROTKRVLETVDHVLOKLRKVTYDERNGREASDNLAQNKGFSN 1518  
Db 616 GSHVKVSKFEKEROTKRVLETVDHVLOKLRKVTYDERNGREASDNLAQNKGFSN 675  
QY 1519 ASGLFEIHGATVPIVSVLAPEKLSASTRRRYETQVQTRLOTSLANLHOKSSEIEILAVD 1578  
Db 676 ASGLFEIHGATVPIVSVLAPEKLSASTRRRYETQVQTRLOTSLANLHOKSSEIEILAVD 735  
QY 1579 LPKETILQFLSLEWDADEQAFNTTVKOLLRLPKQRYLKLVCDEIYNIKVEKKVSVFLY 1638  
Db 736 LPKETILQFLSLEWDADEQAFNTTVKOLLRLPKQRYLKLVCDEIYNIKVEKKVSVFLY 795  
QY 1639 SYRDD 1643  
Db 796 SYRDD 800

RESULT 4  
Q9UJ56

ID Q9UJ56 PRELIMINARY; PRT: 548 AA.  
AC Q9UJ56;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)  
DE PUTATIVE EIF2 ALPHA KINASE (FRAGMENT).  
GN GCN2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99435990; PubMed=10504407;  
RA Berlanga J.J., Santoyo J., de Haro C.;  
RT "Characterization of a mammalian homolog of the GCN2 eukaryotic  
RT Initiation factor 2alpha kinase."  
RL Eur. J. Biochem. 265:754-762(1999).  
DR EMBL: AJ243428; CAB58360.1; -  
KW Kinase.  
FT NON\_TER 1  
SQ SEQUENCE 548 AA; 62759 MW; CB749A9A0F486F0E CRC64;  
  
Query Match 31.0%; Score 510; DB 4; Length 548;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1134 LKRYCIERFPRKLDLPHFHPKELLECADFIVTSTNSFLPTABIIYIYIEIIQEFPAQOE 1193  
Db 33 LKRYCIERFPRKLDLPHFHPKELLECADFIVTSTNSFLPTABIIYIYIEIIQEFPAQOE 92  
  
QY 1194 RNYSIYLNHTMLKAILLHCGIPEDKLSQVYIILYDAVTEKLTRREVEAKFCNLSNSNS 1253  
Db 93 RNYSIYLNHTMLKAILLHCGIPEDKLSQVYIILYDAVTEKLTRREVEAKFCNLSNSNS 152  
  
QY 1254 LCRLYKFEIQKGLDQLMPTINSLIKTGIAQLVYGLKDEEVYGLKLGKIKQLVLI 1313  
Db 153 LCRLYKFEIQKGLDQLMPTINSLIKTGIAQLVYGLKDEEVYGLKLGKIKQLVLI 212  
  
QY 1314 NLGLVYKVOQHNGIIFQVAFIKRRRAVPEILAAAGRYDILLIPQFRGPALGPVPTAIG 1373  
Db 213 NLGLVYKVOQHNGIIFQVAFIKRRRAVPEILAAAGRYDILLIPQFRGPALGPVPTAIG 272  
  
QY 1374 VSIADKISAALNMEESVITSSCDLLVSVGQMSRAINLTQKLTAGITAEIMYDWS 1433  
Db 273 VSIADKISAALNMEESVITSSCDLLVSVGQMSRAINLTQKLTAGITAEIMYDWS 332  
  
QY 1434 QSQELQYCRHHEITVALVSDKESHVVKVSKFERQTEKRVLETDLVHVLQKLRTK 1493  
Db 333 QSQELQYCRHHEITVALVSDKESHVVKVSKFERQTEKRVLETDLVHVLQKLRTK 392  
  
QY 1494 VTDNRNGREASDNLAVONLKGFSNASGLFEIHGATVVPVIVSVLAPEKLSASTRRRYETQ 1553  
Db 393 VTDNRNGREASDNLAVONLKGFSNASGLFEIHGATVVPVIVSVLAPEKLSASTRRRYETQ 452  
  
QY 1554 VOTRLQTSANLHOKSSEIEILAVLPKETILOFLSLEWDADQAFNTTVKQLLSRLPKQ 1613  
Db 453 VOTRLQTSANLHOKSSEIEILAVLPKETILOFLSLEWDADQAFNTTVKQLLSRLPKQ 512  
  
QY 1614 RYLKLVCDIYNIKVEKKSIVFLYSYRDD 1643  
Db 513 RYLKLVCDIYNIKVEKKSIVFLYSYRDD 542  
  
RESULT 5  
Q9NSZ5 PRELIMINARY; PRT; 191 AA.  
AC Q9NSZ5  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DE HYPOTHETICAL 22.1 KDA PROTEIN (FRAGMENT).  
GN DKFPZ434P0612.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=TESTIS;  
RA Duisterhoef A., Lauber J., Mewes H.W., Gassenhuber J., Wiemann S.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL137627; CAB70849.1; -  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 191 AA; 22058 MW; B2032DAEF981C23E CRC64;  
  
Query Match 11.3%; Score 185; DB 4; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.3e-182;  
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1459 GSHVVKVSKFERQTEKRVLETDLVHVLQKLRTKVTDNRNGREASDNLAVONLKGFSFN 1518  
Db 1 GSHVVKVSKFERQTEKRVLETDLVHVLQKLRTKVTDNRNGREASDNLAVONLKGFSFN 60  
  
QY 1519 ASGLFEIHGATVVPVIVSVLAPEKLSASTRRRYETQVQTRLOTSANLHOKSSEIEILAVD 1578  
Db 61 ASGLFEIHGATVVPVIVSVLAPEKLSASTRRRYETQVQTRLOTSANLHOKSSEIEILAVD 120  
  
QY 1579 LPKETILOFLSLEWDADQAFNTTVKQLLSRLPKQRYLKLVCDEIYNIKVEKKSIVFLY 1638  
Db 121 LPKETILOFLSLEWDADQAFNTTVKQLLSRLPKQRYLKLVCDEIYNIKVEKKSIVFLY 180  
  
QY 1639 SYRDD 1643  
Db 181 SYRDD 185  
  
RESULT 6  
Q9QZ05 PRELIMINARY; PRT; 1648 AA.  
AC Q9QZ05  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE GCN2 EIF2ALPHA KINASE.  
GN EIF2AK4 OR GCN2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RX MEDLINE=99435990; PubMed=10504407;  
RA Berlanga J.J., Santoyo J., de Haro C.;  
RT "Characterization of a mammalian homolog of the GCN2 eukaryotic  
RT Initiation factor 2alpha kinase."  
RL Eur. J. Biochem. 265:754-762(1999).  
CC -!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL: AJ243427; CAB58363.1; -  
DR MGD; MGI:1353427; Eif2ak4.  
DR InterPro; IPR000719; -  
DR InterPro; IPR002290; -  
DR Pfam; PF00069; pkinase; 4.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 2.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR SMART; SM00221; STYKc; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 1648 AA; 186513 MW; F27CBBAB31DD39B CRC64;  
  
Query Match 5.2%; Score 85; DB 11; Length 1648;  
Best Local Similarity 100.0%; Pred. No. 2.8e-78;  
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1395 SSCDLLVSVGQMSRAINLTQKLTAGITAEIMYDWSQSQELQYCRHHEITVALV 1454

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Db 1394 SSCDLLVSVGQMSRAINTQKLTAGITAEIMYDWSQSEELQCYCRHHITYVALV 1453
QY 1455 SDKEGSHVKVKSFEKEROTKRVLE 1479
Db 1454 SDKEGSHVKVKSFEKEROTKRVLE 1478

RESULT 7
Q9ESB8 PRELIMINARY; PRT; 1370 AA.
AC Q9ESB8;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE GCN2ALPHA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20157056; PubMed=10655230;
RA Sood R., Porter A.C., Olsen D.A., Cavener D.R., Wek R.C.;
RT "A mammalian homologue of GCN2 protein kinase important for
RT translational control by phosphorylation of eukaryotic initiation
RT factor-2alpha."
RL Genetics 154:787-801(2000).
DR EMBL; AF193342; AAG22589.1; -.
SQ SEQUENCE 1370 AA; 154854 MW; AAF8A7C22608681E CRC64;

Query Match 5.0%; Score 82; DB 11; Length 1370;
Best Local Similarity 100.0%; Pred. No. 3.1e-75;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1562 LANLHOKSSEIEILAVDLPKETILQFLSLEWDADQAFNTTVKQLLSRLPKORYLKLVCD 1621
Db 1283 LANLHOKSSEIEILAVDLPKETILQFLSLEWDADQAFNTTVKQLLSRLPKORYLKLVCD 1342

QY 1622 EYINIKVEKKVSVLFYSYRDD 1643
Db 1343 EYINIKVEKKVSVLFYSYRDD 1364

RESULT 8
Q9ESB6 PRELIMINARY; PRT; 1570 AA.
AC Q9ESB6;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE GCN2GAMMA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20157056; PubMed=10655230;
RA Sood R., Porter A.C., Olsen D.A., Cavener D.R., Wek R.C.;
RT "A mammalian homologue of GCN2 protein kinase important for
RT translational control by phosphorylation of eukaryotic initiation
RT factor-2alpha."
RL Genetics 154:787-801(2000).
DR EMBL; AF193344; AAG22591.1; -.
SQ SEQUENCE 1570 AA; 177825 MW; 00E3B8D7E926D130 CRC64;

Query Match 5.0%; Score 82; DB 11; Length 1570;
Best Local Similarity 100.0%; Pred. No. 3.5e-75;
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Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1562 LANLHOKSSEIEILAVDLPKETILQFLSLEWDADQAFNTTVKQLLSRLPKORYLKLVCD 1621
Db 1483 LANLHOKSSEIEILAVDLPKETILQFLSLEWDADQAFNTTVKQLLSRLPKORYLKLVCD 1542

QY 1622 EYINIKVEKKVSVLFYSYRDD 1643
Db 1543 EYINIKVEKKVSVLFYSYRDD 1564

RESULT 9
Q9ESB7 PRELIMINARY; PRT; 1648 AA.
AC Q9ESB7;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE GCN2BETA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20157056; PubMed=10655230;
RA Sood R., Porter A.C., Olsen D.A., Cavener D.R., Wek R.C.;
RT "A mammalian homologue of GCN2 protein kinase important for
RT translational control by phosphorylation of eukaryotic initiation
RT factor-2alpha."
RL Genetics 154:787-801(2000).
DR EMBL; AF193343; AAG22590.1; -.
SQ SEQUENCE 1648 AA; 186393 MW; 95AE7BE40C3F7ADA CRC64;

Query Match 5.0%; Score 82; DB 11; Length 1648;
Best Local Similarity 100.0%; Pred. No. 3.6e-75;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1562 LANLHOKSSEIEILAVDLPKETILQFLSLEWDADQAFNTTVKQLLSRLPKORYLKLVCD 1621
Db 1561 LANLHOKSSEIEILAVDLPKETILQFLSLEWDADQAFNTTVKQLLSRLPKORYLKLVCD 1620

QY 1622 EYINIKVEKKVSVLFYSYRDD 1643
Db 1621 EYINIKVEKKVSVLFYSYRDD 1642

RESULT 10
Q61651 PRELIMINARY; PRT; 1589 AA.
AC Q61651;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE EIF-2ALPHA KINASE.
GN GCN2 OR CG1609.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON R;
RA Olsen D.S., Jordan B., Chen D., Cavener D.R.;
RL Genetics 0:0-0(1998).
CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF056302; AAC13490.1; -.
DR FlyBase; FBgn0019990; Gcn2.
DR InterPro; IPR000719; -.
DR InterPro; IPR002290; -.
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DR Pfam: PF00069; pkinase; 3.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR SMART: SM00220; S\_TKc; 1.  
 KW ATP-binding; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 1589 AA; 178689 MW; 4CBF2CE6C656D906 CRC64;

Query Match 0.9%; Score 14; DB 5; Length 1589;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 845 IHRDLKPNVIFLDS 858  
 |||||  
 Db 741 IHRDLKPNVIFLDS 754

RESULT 11

ID 001712 PRELIMINARY; PRT; 1589 AA.

AC 001712;

DT 01-JUL-1997 (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE EUKARYOTIC INITIATION FACTOR EIF-2 ALPHA KINASE.

GN GCN2 OR CG1609.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

FN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-97284729; PubMed-9139706;

RA Santoyo J., Alcalde J., Mendez R., Pulido D., de Haro C.;

RT "Cloning and characterization of a cDNA encoding a protein synthesis

RT initiation factor-2alpha (eif-2alpha) kinase from Drosophila

RT melanogaster. Homology to yeast GCN2 protein kinase.";

RL J. Biol. Chem. 272.12544-12550(1997).

CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; U80223; AAC47516.1;

DR FlyBase; FBgn0019990; Gcn2.

DR InterPro; IPR000719;

DR InterPro; IPR002290;

DR Pfam; PF00069; pkinase; 3.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

DR SMART; SM00220; S\_TKc; 1.

KW ATP-binding; Initiation factor; Serine/threonine-protein kinase;

KW Transferase.

SQ SEQUENCE 1589 AA; 178708 MW; CB5D8086978883C1 CRC64;

Query Match 0.9%; Score 14; DB 5; Length 1589;

Best Local Similarity 100.0%; Pred. No. 9.2e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 845 IHRDLKPNVIFLDS 858

|||||

Db 741 IHRDLKPNVIFLDS 754

RESULT 12

ID Q9V9X8 PRELIMINARY; PRT; 1589 AA.

AC Q9V9X8;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE GCN2 PROTEIN.

GN GCN2 OR CG1609.

OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;

FN [1]

RP SEQUENCE FROM N.A.

RX STRAIN-BERKELEY;

RX MEDLINE-20196006; PubMed-10731132;

RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,

RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; AE003778; AAF57150.1;

DR FlyBase; FBgn0019990; Gcn2.

DR InterPro; IPR000719;

DR InterPro; IPR002290;

DR Pfam; PF00069; pkinase; 3.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

DR SMART; SM00220; S\_TKc; 1.

KW ATP-binding; Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 1589 AA; 178680 MW; 5220188688C9BD36 CRC64;

Query Match 0.9%; Score 14; DB 5; Length 1589;

Best Local Similarity 100.0%; Pred. No. 9.2e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 845 IHRDLKPNVIFLDS 858

|||||

Db 741 IHRDLKPNVIFLDS 754

RESULT 13

Q9V9X8

ID Q9V9X8 PRELIMINARY; PRT; 576 AA.

Q9VNB2;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)  
 DE POLO PROTEIN  
 GN POLO OR CGI2306.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 RN NCBI\_TaxID=7227;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Arlil J.F., Aghayani A., An H.-J., Andrews-pfannkuch C., Baldwin D.,  
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.V., Benos P.V., Berman B.P., Brandler D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RA "The genome sequence of Drosophila melanogaster."  
 RT Science 287:2185-2195(2000).  
 CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AE003514; AAF49036.1;  
 DR FlyBase; FBgn003124; polo.  
 DR InterPro; IPR000719;  
 DR InterPro; IPR000959;  
 DR InterPro; IPR002290;  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00659; POLO\_box; 2.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 KW ATP-binding; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 576 AA; 66973 MW; 5022B9AC0E888FAD CRC64;

Query Match 0.7%; Score 11; DB 5; Length 576;  
 Best Local Similarity 100.0%; Pred. No. 0.051;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 861 HVKIGDFGLAT 871

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 Db 161 HVKIGDFGLAT 171  
 RESULT 14  
 Q9DEB2 PRELIMINARY; PRT; 285 AA.  
 ID O3DEB2  
 AC O3DEB2  
 DT 01-MAR-2001 (TREMELrel. 16, Created)  
 DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)  
 DE CRAF PROTEIN (FRAGMENT).  
 GN CRAF.  
 OS Seriola quinqueradiata (Five-ray yellowtail).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Perciformes; Carangoidae;  
 OC Carangidae; Seriola.  
 RN NCBI\_TaxID=8161;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=GILL;  
 RA Doi M., Abe S.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=GILL;  
 RA Gray T.A., Azama K., Whitmore K.L., Min A., Abe S., Nicholls R.D.;  
 RA "A conserved gene antisense to the proto-oncogene c-Raf encodes a  
 RT multi-zinc-finger protein, MAKORIN2."  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB049965; BAB18860.1;  
 FT NON\_TER  
 SQ SEQUENCE 285 AA; 32519 MW; 99A692B08A9D4668 CRC64;  
 Query Match 0.6%; Score 10; DB 13; Length 285;  
 Best Local Similarity 100.0%; Pred. No. 0.31;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 862 VKIGDFGLAT 871  
 Db 120 VKIGDFGLAT 129  
 RESULT 15  
 O19055 PRELIMINARY; PRT; 301 AA.  
 ID O19055  
 AC O19055  
 DT 01-JAN-1998 (TREMELrel. 05, Created)  
 DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)  
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)  
 DE C-RAP HOMOLOG (FRAGMENT).  
 OS Papio hamadryas (Hamadryas baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Papio.  
 RN NCBI\_TaxID=9557;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RA Mandiyan S., Schumacher C., Cioffi C., Sharif H., Yuryev A., Lappe R.,  
 RA Monia B., Hanson S., Goff S., Wennog L.P.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AF006463; AAB63196.1;  
 DR HSP; P06239; 3LCK.  
 DR InterPro; IPR000719;  
 DR InterPro; IPR001245;  
 DR InterPro; IPR002290;  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR SMART: SM00220; S\_TKc; 1.  
 KW ATP-binding; Serine/threonine-protein kinase; Transferase;  
 KW Tyrosine-protein kinase.  
 FT NON\_TER 1  
 SQ SEQUENCE 301 AA; 34230 MW; 3512983ADF5D1A3B CRC64;

Query Match 0.6%; Score 10; DB 6; Length 301;  
 Best Local Similarity 100.0%; Pred. NO. 0.33;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 862 VKIGDFGLAT 871  
 Db 135 VKIGDFGLAT 144

Search completed: October 22, 2001, 01:31:30  
 Job time: 271 sec